Fig. 1A

```
   1 GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG ATTTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC
     CGACACCCTT GGAGAGGTGC GCGTGCTTGA GTCGGTTGCT AAAGACTATC TAAAAACCCT CAAACTGGTC TCTACGTTCC CCACTTCCTC GCGAAGGATG

 101 CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCATA CCATGGCCCG
     GCAATCCCTT GAGACCCCTG TCTCGCGGGG CCGGCGGACT ACCGGCTCCG TCCCACGCTG GGTCCTGGGT CCTGCCGCAG CCCTTGGTAT GGTACCGGGC
   1                                                                                                   MetAlaArg

 201 GATCCCCAAG ACCCTAAAGT TCGTCGTCGT CATCGTCGCG GTCCTGCTGC CAGTCCTAGC TTACTCTGCC ACCACTGCCC GGCAGGAGGA AGTTCCCCAG
     CTAGGGGTTC TGGGATTTCA AGCAGCAGCA GTAGCAGCGC CAGGACGACG GTCAGGATCG AATGAGACGG TGGTGACGGG CCGTCCTCCT TCAAGGGGTC
     4  IleProLys ThrLeuLysP heValValVa lIleValAla ValLeuLeuP roValLeuAl aTyrSerAla ThrThrAlaA rgGlnGluGl uValProGln

 301 CAGACAGTGG CCCCACAGCA ACAGAGGCAC AGCTTCAAGG GGGAGGAGTG TCCAGCAGGA TCTCATAGAT CAGAACATAC TGGAGCCTGT AACCCGTGCA
     GTCTGTCACC GGGGTGTCGT TGTCTCCGTG TCGAAGTTCC CCCTCCTCAC AGGTCGTCCT AGAGTATCTA GTCTTGTATG ACCTCGGACA TTGGGCACGT
    37 GlnThrValA laProGlnGl nGlnArgHis SerPheLysG lyGluGluCy sProAlaGly SerHisArgS erGluHisTh rGlyAlaCys AsnProCysThr

 401 CAGAGGGTGT GGATTACACC AACGCTTCCA ACAATGAACC TTCTTGCTTC CCATGTACAG TTTGTAAATC AGATCAAAAA CATAAAAGTT CCTGCACCAT
     GTCTCCCACA CCTAATGTGG TTGCGAAGGT TGTTACTTGG AAGAACGAAG GGTACATGTC AAACATTTAG TCTAGTTTTT GTATTTTCAA GGACGTGGTA
    71   GluGlyVa lAspTyrThr AsnAlaSerA snAsnGluPr oSerCysPhe ProCysThrV alCysLysSe rAspGlnLys HisLysSerS erCysThrMet

 501 GACCAGAGAC ACAGTGTGTC AGTGTAAAGA AGGCACCTTC CGGAATGAAA ACTCCCCAGA GATGTGCCGG AAGTGTAGCA GGTGCCCTAG TGGGGAAGTC
     CTGGTCTCTG TGTCACACAG TCACATTTCT TCCGTGGAAG GCCTTACTTT TGAGGGGTCT CTACACGGCC TTCACATCGT CCACGGGATC ACCCCTTCAG
   104  ThrArgAsp ThrValCysG lnCysLysGl uGlyThrPhe ArgAsnGluA snSerProGl uMetCysArg LysCysSerA rgCysProSe rGlyGluVal

 601 CAAGTCAGTA ATTGTACGTC CTGGGATGAT ATCCAGTGTG TTGAAGAATT TGGTGCCAAT GCCACTGTGG AAACCCCAGC TGCTGAAGAG ACAATGAACA
     GTTCAGTCAT TAACATGCAG GACCCTACTA TAGGTCACAC AACTTCTTAA ACCACGGTTA CGGTGACACC TTTGGGGTCG ACGACTTCTC TGTTACTTGT
   137 GlnValSerA snCysThrSe rTrpAspAsp IleGlnCysV alGluGluPh eGlyAlaAsn AlaThrValG luThrProAl aAlaGluGlu ThrMetAsnThr

 701 CCAGCCCGGG GACTCCTGCC CCAGCTGCTG AAGAGACAAT GAACACCAGC CCAGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGGG
     GGTCGGGCCC CTGAGGACGG GGTCGACGAC TTCTCTGTTA CTTGTGGTCG GGTCCCTGAG GACGGGGTCG ACGACTTCTC TGTTACTGGT GGTCGGGCCC
   171   SerProGl yThrProAla ProAlaAlaG luGluThrMe tAsnThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGly

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     CTGAGGACGG GGTCGACGAC TTCTCTGTTA CTGGTGGTCG GGCCCCTGAG GACGGGGTCG ACGACTTCTC TGTTACTGGT GGTCGGGCCC CTGAGGACGG
   204  ThrProAla ProAlaAlaG luGluThrMe tThrThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGl yThrProAla

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     AGAAGAGTAA TGGAGAGTAC GTGGTAGCAT CCCTAGTATC AAGATTAACA CGAAGACTAA CACAAACAAA CTTTCTGAAG TGACACCTTC TTTAAGGAAG
   237 SerSerHisT yrLeuSerCy sThrIleVal GlyIleIleV alLeuIleVa lLeuLeuIle ValPheVal

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Fig. 1B

```
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    CGACACCCTT GGAGAGGTGC GCGTGCTTGA GTCGGTTGCT AAAGACTATC TAAAAACCCT CAAACTGGTC TCTACGTTCC CCACTTCCTC GCGAAGGATG
-40                                                                                                  MetGlnGl yValLysGlu ArgPheLeuPro

101 CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCATA CCATGGCCCG
    GCAATCCCTT GAGACCCCTG TCTCGCGGGG CCGGCGGACT ACCGGCTCCG TCCCACGCTG GGTCCTGGGT CCTGCCGCAG CCCTTGGTAT GGTACCGGGC
-30   LeuGlyAs nSerGlyAsp ArgAlaProA rgProProAs pGlyArgGly ArgValArgP roArgThrGl nAspGlyVal GlyAsnHisT hrMetAlaArg

201 GATCCCCAAG ACCCTAAAGT TCGTCGTCGT CATCGTCGCG GTCCTGCTGC CAGTCCTAGC TTACTCTGCC ACCACTGCCC GGCAGGAGGA AGTTCCCCAG
    CTAGGGGTTC TGGGATTTCA AGCAGCAGCA GTAGCAGCGC CAGGACGACG GTCAGGATCG AATGAGACGG TGGTGACGGG CCGTCCTCCT TCAAGGGGTC
  4  IleProLys ThrLeuLysP heValValVa lIleValAla ValLeuLeuP roValLeuAl aTyrSerAla ThrThrAlaA rgGlnGluGl uValProGln

301 CAGACAGTGG CCCCACAGCA ACAGAGGCAC AGCTTCAAGG GGGAGGAGTG TCCAGCAGGA TCTCATAGAT CAGAACATAC TGGAGCCTGT AACCCGTGCA
    GTCTGTCACC GGGGTGTCGT TGTCTCCGTG TCGAAGTTCC CCCTCCTCAC AGGTCGTCCT AGAGTATCTA GTCTTGTATG ACCTCGGACA TTGGGCACGT
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    CTGGTCTCTG TGTCACACAG TCACATTTCT TCCGTGGAAG GCCTTACTTT TGAGGGGTCT CTACACGGCC TTCACATCGT CCACGGGATC ACCCCTTCAG
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    GTTCAGTCAT TAACATGCAG GACCCTACTA TAGGTCACAC AACTTCTTAA ACCACGGTTA CGGTGACACC TTTGGGGTCG ACGACTTCTC TGTTACTTGT
137 GlnValSerA snCysThrSe rTrpAspAsp IleGlnCysV alGluGluPh eGlyAlaAsn AlaThrValG luThrProAl aAlaGluGlu ThrMetAsnThr

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Apo2DcR     1   ---------------------------------------MARIPKTLKFVV
DR4        51   GRGALPTSMGQHGPSARARAGRAPGPRPAREASPRLRVHKTFKFVVVGVL

Apo2       41   VVAAVLLLVSAESALITQQDLAPQQRAAPQQKRSSPSEGLCPPGHHISED
Apo2DcR    13   VIVAVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEH
DR4       101   LQVVPSSAATIK---------LHDQSIGTQQWEHSPLGELCPPGSHRSER

                                       CRD1
Apo2       91   GRDCISCKYGQDYSTHWNDLLFCLRCTRCDSGEVELSPCTTTRNTVCQCE
Apo2DcR    63   TGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCK
DR4       142   PGACNRCTEGVGYTNASNNLFACLPCTACKSDEEERSPCTTTRNTACQCK

                                 CRD2
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Apo2DcR   113   EGTFRNENSPEMCRKCSR-CPSGEVQVSNCTSWDDIQCVE-EFGANATVE
DR4       192   PGTFRNDNSAEMCRKCSTGCPRGMVKVKDCTPWSDIECVHKE--------

Apo2            --------------------------------------------------
Apo2DcR   161   TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAE
DR4             --------------------------------------------------

Apo2      183   ---------------------------SGIIIGVTVAAVVLIVAVFV---
Apo2DcR   211   ETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLLIVFV
DR4       234   ---------------------SGNGHNIWVILVVTLVVPLLLVAV-LIVC

Apo2      203   CKSLLWKKVLPYLKGICSGGGGDPERVDRSSQRPGAEDNVLNEIVSILQP
DR4       262   CCIGSGCGGDPKCMDRVCFWRLGLLRGPGAEDNAHNEILSNADSLSTFVS

Apo2      253   TQVPEQEMEVQEPAEPTGVNMLSPGESEHLLEPAEAERSQRRRLLVPANE
DR4       312   ----EQQMESQEPADLTGVTVQSPGEAQCLLGPAEAEGSQRRRLLVPANG

Apo2      303   GDPTETLRQCFDDFADLVPFDSWEPLMRKLGLMDNEIKVAKAEAAGH--R
DR4       358   ADPTETLMLFFDKFANIVPFDSWDQLMRQLDLTKNEIDVVRAGTAGP--G
Apo3/DR3  338                        VMDAVPARRWKEFVRTLGLREAEIEAVEVEI-GRF-R
TNFR1     322                        VVENVPPLRWKEFVRRLGLSDHEIDRLELQN-GRCLR
CD95      220                        IAGVHTLSQVKGFVRKNGVNEAKIDEIKNDN-VQDTA

Apo2      351   DTLYTMLIKWVNKTGR-DASVHTLLDALETLGERLAKQKIEDHLLSSGKF
DR4       406   DALYAMLMKWVNKTGR-NASIHTLLDALERMEERHAKEKIQDLLVDSGKF
Apo3/DR3  374   DQQYEMLKRWRQQQP---AGLGAVYAALERMGLDGCVEDLRS
TNFR1     358   EAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEE
CD95      256   EQKVQLLRNWHQLHGKKEAY-DTLIKDLKKANLCTLAEKIQT

Apo2      400   MYLEGNADSALS
DR4       455   IYLEDGTGSAVSLE
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Fig. 2

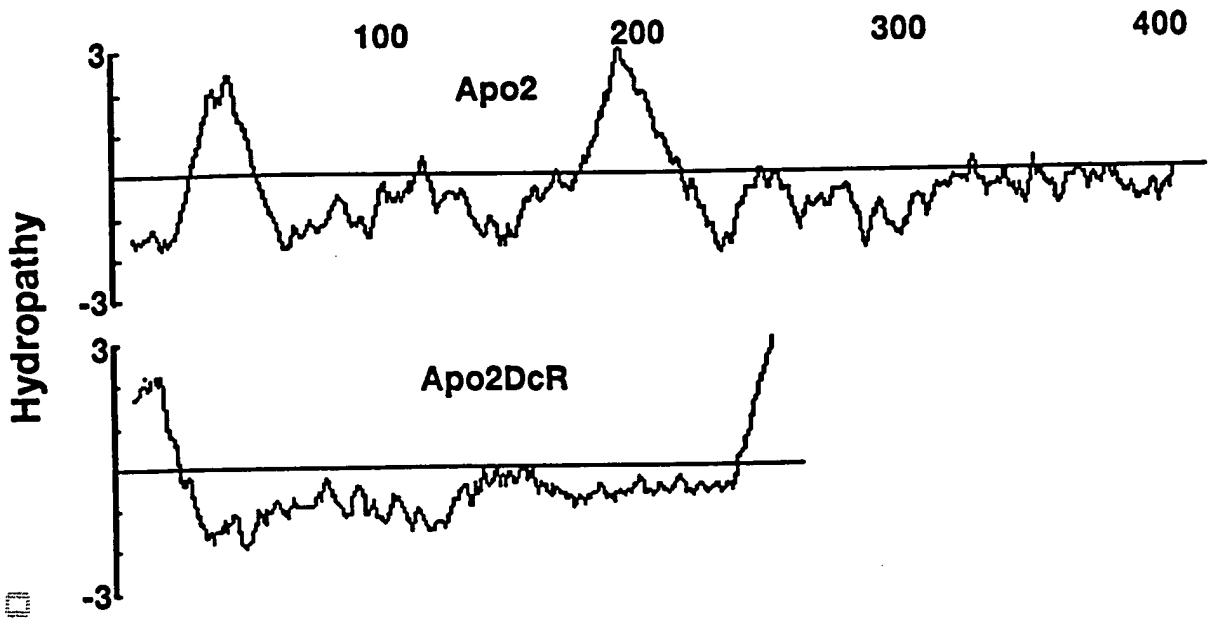

Figure 3

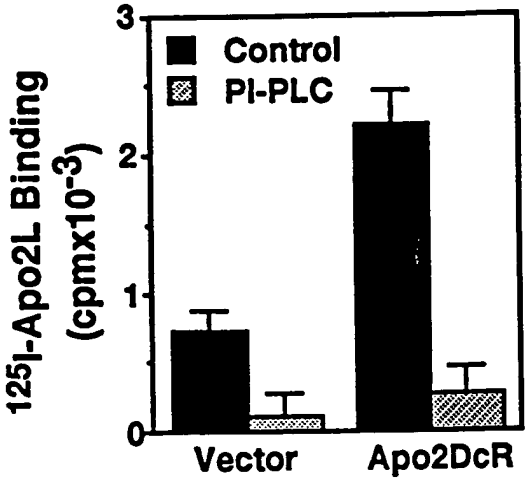
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Figure 4

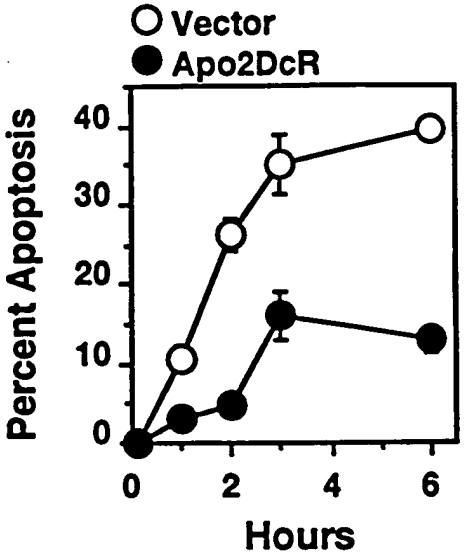

Figure 5

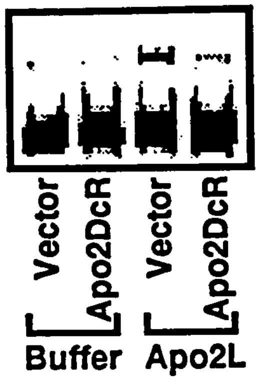

Figure 6

Fig. 7A

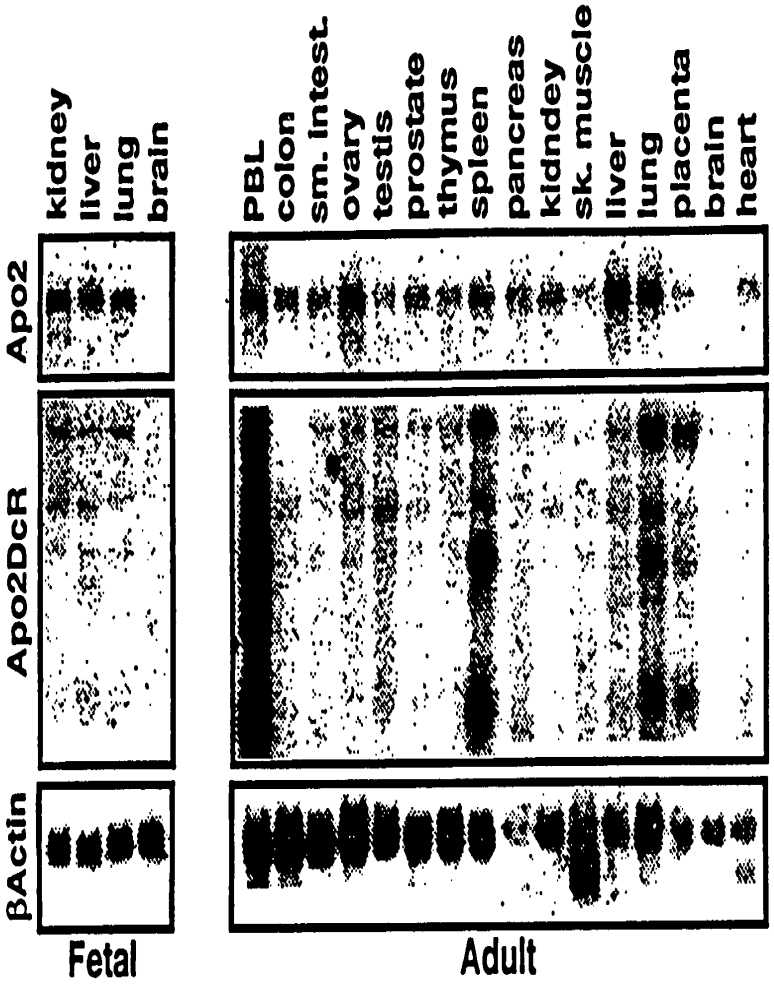

Fig. 7B

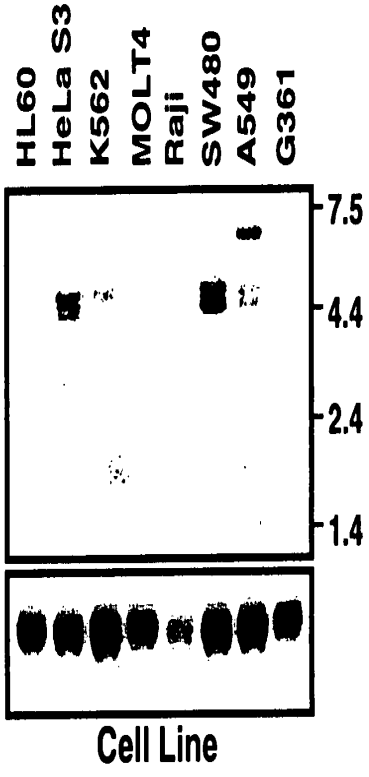

Fig. 8

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     GGGTGCGCAG GCGTATTTAG TCGTGCGCCG GCCTCTTGGG GCGTTAGAGA CGCGGGTGTT TTATGTGGCT GCTACGGGCT AGATGAAATT CCCGACTTTG

 101 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCCA TGGAACAACG GGGACAGAAC GCCCCGGCCG CTTCGGGGGC CCGGAAAAGG CACGGCCCAG
     GGTGCCCGGA CTCTCTGATA TTCTCGCAAG GGATGGCGGT ACCTTGTTGC CCCTGTCTTG CGGGGCCGGC GAAGCCCCCG GGCCTTTTCC GTGCCGGGTC
   1                                       M etGluGlnAr gGlyGlnAsn AlaProAlaA laSerGlyAl aArgLysArg HisGlyProGly

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     CTGGGTCCCT CCGCGCCCCT CGGTCCGGAC CCGAGGCCCA GGGGTTCTGG GAACACGAGC AACAGCGGCG CCAGGACGAC AACCAGAGTC GACTCAGACG
  22   ProArgGl uAlaArgGly AlaArgProG lyLeuArgVa lProLysThr LeuValLeuV alValAlaAl aValLeuLeu LeuValSerA laGluSerAla

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  55  LeuIleThr GlnGlnAspL euAlaProGl nGlnArgAla AlaProGlnG lnLysArgSe rSerProSer GluGlyLeuC ysProProGl yHisHisIle

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     AGTCTTCTGC CATCTCTAAC GTAGAGGACG TTTATACCTG TCCTGATATC GTGAGTGACC TTACTGGAGG AAAAGACGAA CGCGACGTGG TCCACACTAA
  88 SerGluAspG lyArgAspCy sIleSerCys LysTyrGlyG lnAspTyrSe rThrHisTrp AsnAspLeuL euPheCysLe uArgCysThr ArgCysAspSer

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     CTTCACGGCG TGTCCCACAG GGTCTCCCTA CCAGTTCCAG CCACTAACAT GTGGGACCTC ACTGTAGCTT ACACAGGTGT TTCTTAGTCC GTAGTAGTAT
 155  LysCysArg ThrGlyCysP roArgGlyMe tValLysVal GlyAspCysT hrProTrpSe rAspIleGlu CysValHisL ysGluSerGl yIleIleIle

 701 GGAGTCACAG TTGCAGCCGT AGTCTTGATT GTGGCTGTGT TTGTTTGCAA GTCTTTACTG TGGAAGAAAG TCCTTCCTTA CCTGAAAGGC ATCTGCTCAG
     CCTCAGTGTC AACGTCGGCA TCAGAACTAA CACCGACACA AACAAACGTT CAGAAATGAC ACCTTCTTTC AGGAAGGAAT GGACTTTCCG TAGACGAGTC
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     CACCACCACC CCTGGGACTC GCACACCTGT CTTCGAGTGT TGCTGGACCC CGACTCCTGT TACAGGAGTT ACTCTAGCAC TCATAGAACG TCGGGTGGGT
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     CGACTTTCCA GAGTCTCCTC CTCCGACGAC CAAGGTCGTT TACTTCCACT AGGGTGACTC TGAGACTCTG TCACGAAGCT ACTGAAACGT CTGAACCACG
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Fig. 8 (cont.)

FIG. 9

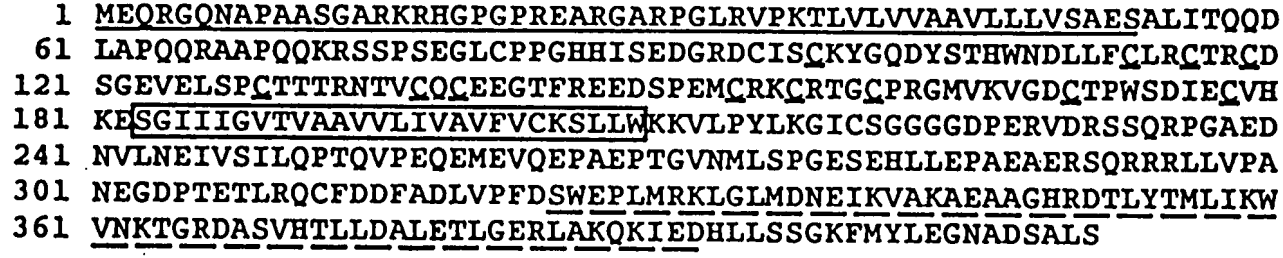


Fig. 10

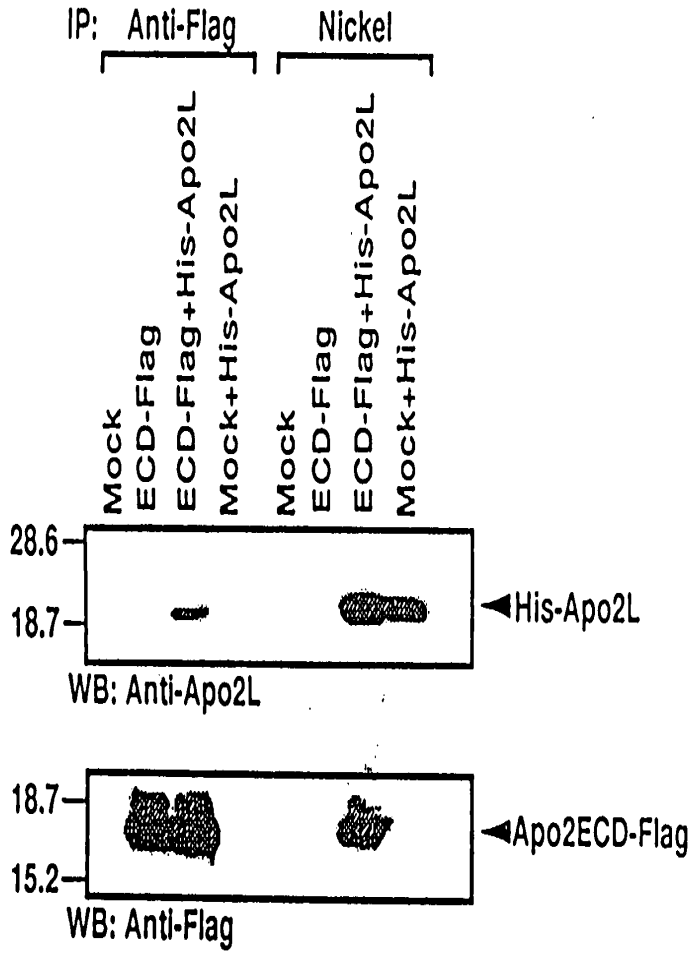
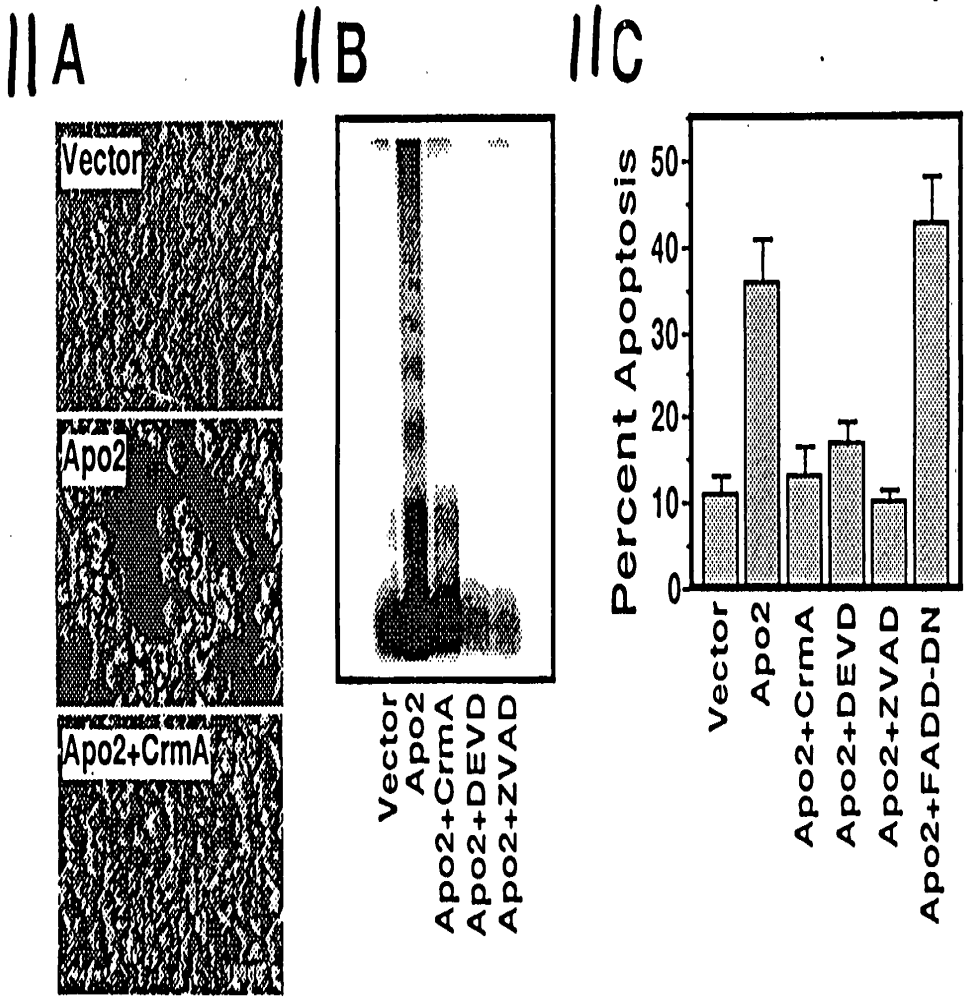
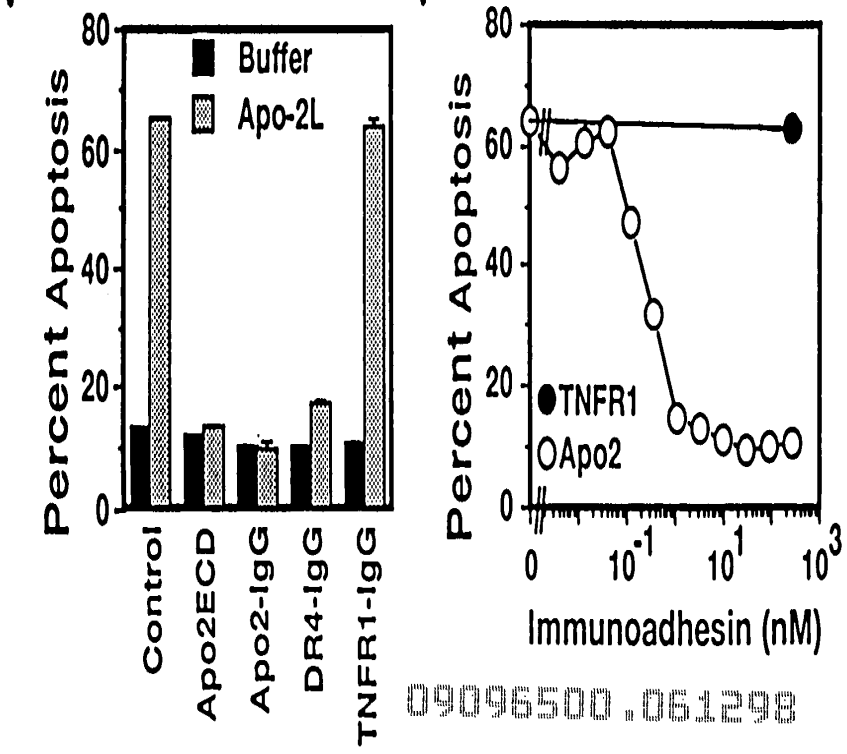
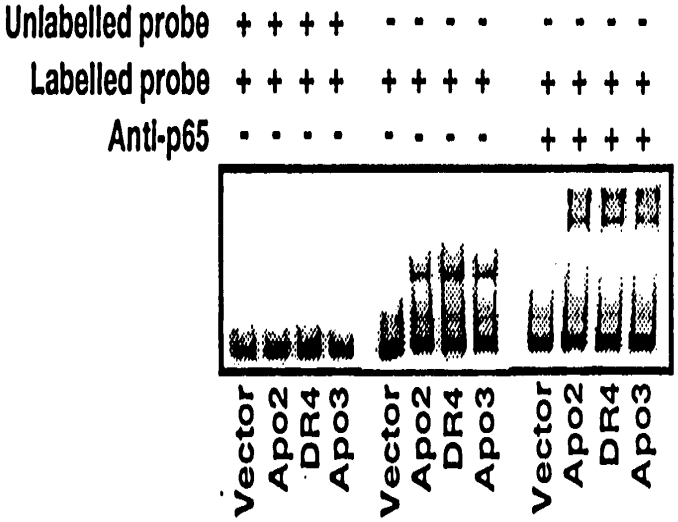


Fig. 11





12A



12B

12C

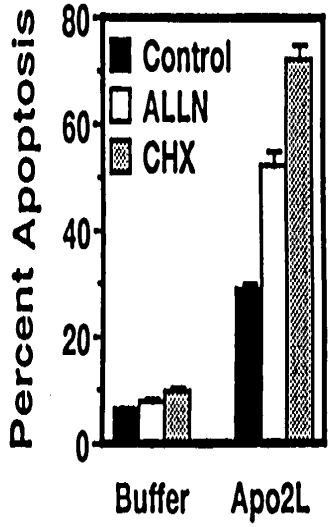


FIG. 12

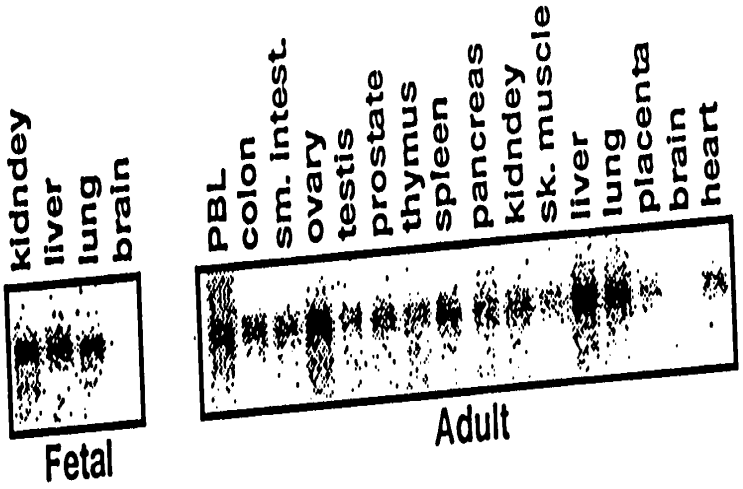
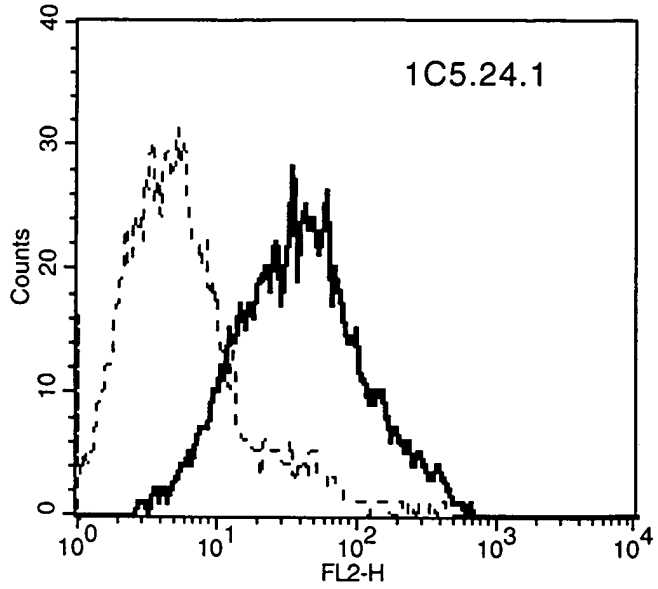
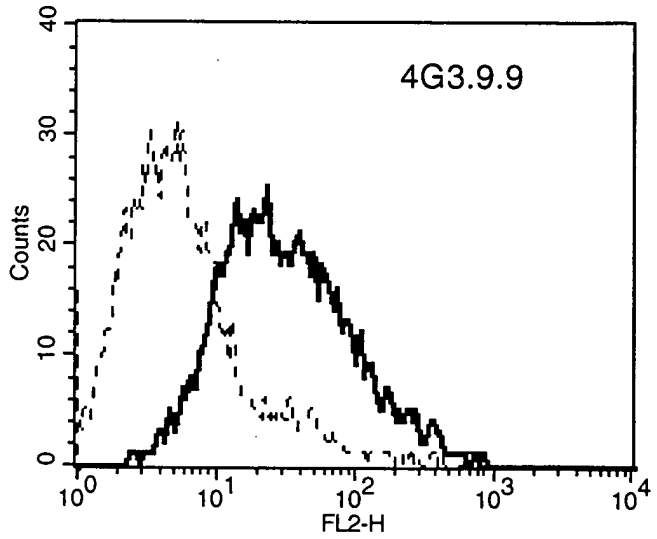


FIG. 13





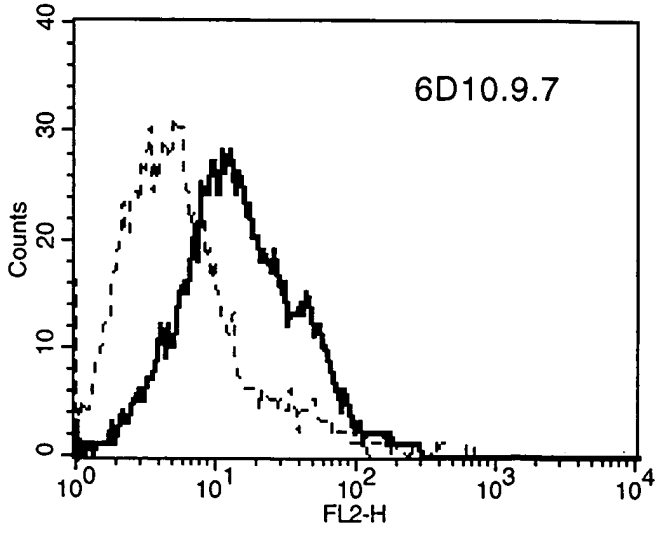
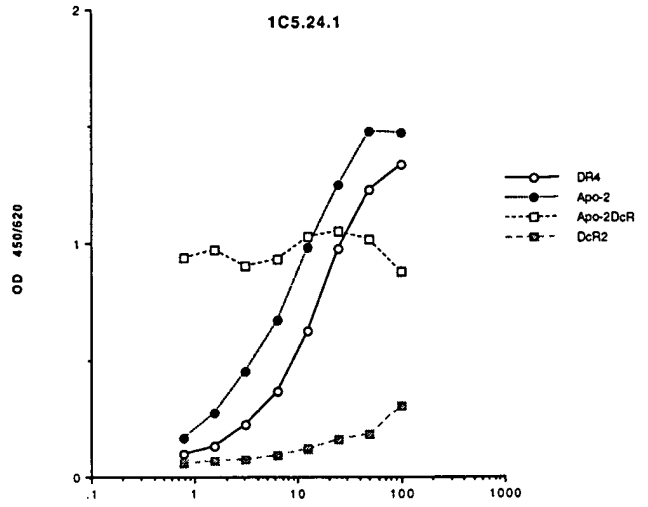
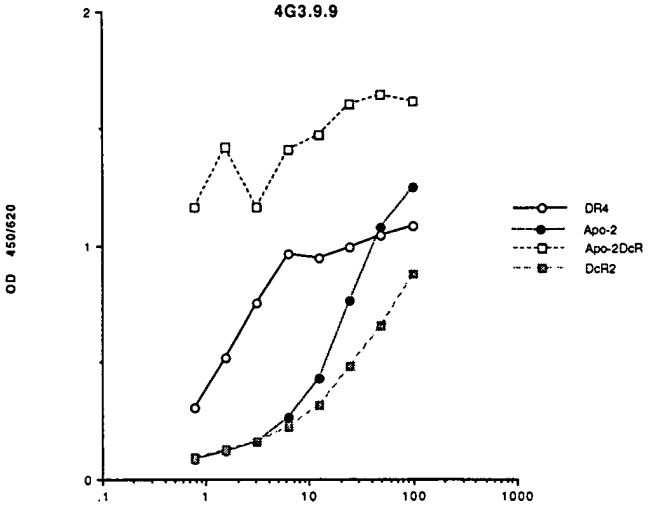


Fig. 14


1C5.24.1
OD 450/620
DR4
Apo-2
Apo-2DcR
DcR2
0
1
2
.1
1
10
100
1000


4G3.9.9
OD 450/620
DR4
Apo-2
Apo-2DcR
DcR2
0
1
2
.1
1
10
100
1000

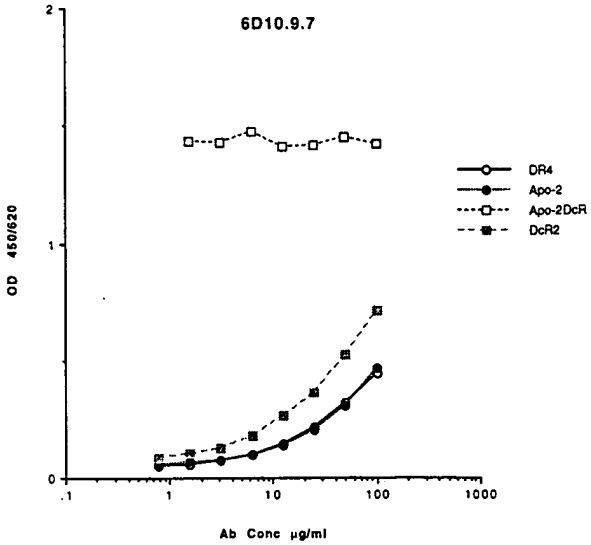

6D10.9.7
OD 450/620
DR4
Apo-2
Apo-2DcR
DcR2
0
1
2
.1
1
10
100
1000
Ab Conc µg/ml

Fig. 15

Summary of mAbs to DcR1

mAbs	ISOTYPE	FACS (HUMEC)	DR4	Cross reactivity Apo-2	Apo-2DcR	DcR2
1C5.24.1	IgG1	+	++	+++	+++	-
4G3.9.9	IgG1	+	++	+	+++	+/-
6D10.9.7	IgG2b	+	-	-	+++	+/-

Percent Cross reactivity was determined by comparing the binding capacity to Apo-2DcR at 10 ug/ml of mAbs in ELISA. ++: >75% , +: 25-75%, +/-:10-25%, -: <10% .

Fig. 16